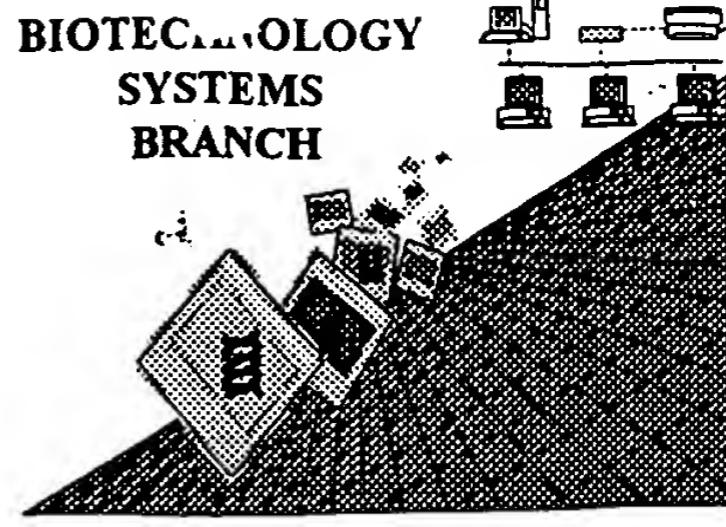


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/765,614A

Source: 1619

Date Processed by STIC: 6/20/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

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Raw Sequence Listing Error Summary

JUL 11 2001

TECH CENTER 1600/2900

SERIAL NUMBER: 09/765,614A

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>
ATTN NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE	
1 <input checked="" type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

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JUL 11 2001

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/765,614ADATE: 06/20/TECH CENTER 1600/2900
TIME: 11:00:39Input Set : A:\64990SEQ.WPD8-31.txt.txt
Output Set: N:\CRF3\06202001\I765614A.raw

6 <110> APPLICANT: Nycomed Imaging AS
 8 <120> TITLE OF INVENTION: Improvements in or relating to
 9 diagnostic/therapeutic
 10 agents
 12 <130> FILE REFERENCE: REF/Klaveness/054C
 OK-> 14 <140> CURRENT APPLICATION NUMBER: US/09/765,614A
 15 <141> CURRENT FILING DATE: 2001-01-22
 E--> 17 <160> NUMBER OF SEQ ID NOS: 25 31 (p. 6)
 19 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
Corrected Diskette Needed

jpr 1-6

ERRORED SEQUENCES

36 <210> SEQ ID NO: 2
 37 <211> LENGTH: 25
 38 <212> TYPE: PRT
 39 <213> ORGANISM: Artificial Sequence
 41 <220> FEATURE:
 42 <223> OTHER INFORMATION: Description of Artificial
 43 Sequence: Peptide → move up
 44 comprising →
 45 phosphatidylserine-binding and →
 W--> 46 heparin-binding sections →
 48 <400> SEQUENCE: 2
 49 Phe Asn Phe Arg Leu Lys Ala Gly Gln
 E--> 50 Lys Ile Arg Phe Gly Ala Ala
 51 1 5 →
 E--> 52 10 15 → see item 1 on
 54 Ala Trp Glu Pro Pro Arg Ala Arg Ile
 E--> 56 20 25 → Error Summary
 127 <210> SEQ ID NO: 7
 128 <211> LENGTH: 13
 129 <212> TYPE: PRT
 130 <213> ORGANISM: Artificial Sequence
 132 <220> FEATURE:
 133 <223> OTHER INFORMATION: Description of Artificial
 134 Sequence: Lipopeptide
 135 consisting of a heparin
 136 sulphate binding peptide
 W--> 137 and a fibronectin peptide →
 139 <220> FEATURE:
 140 <221> NAME/KEY: MOD_RES
 141 <222> LOCATION: (1)
 142 <223> OTHER INFORMATION: Dipalmitoyl-lysine
 144 <400> SEQUENCE: 7
 145 Lys Lys Arg Lys Arg Trp Gln Pro Pro
 E--> 146 Arg Ala Arg Ile →
 move lines up - Per 1823
 of Sequence Rules,
 a MAXIMUM of
 4 lines for <223>
 response
 same error

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/765,614A

DATE: 06/20/2001
TIME: 11:00:39

Input Set : A:\64990SEQ.WPD8-31.txt.txt
Output Set: N:\CRF3\06202001\I765614A.raw

E--> 147 1 5
E--> 148 10
151 <210> SEQ ID NO: 8
152 <211> LENGTH: 24
153 <212> TYPE: PRT
154 <213> ORGANISM: Artificial Sequence
156 <220> FEATURE:
157 <223> OTHER INFORMATION: Description of Artificial
158 Sequence: Fibronectin
159 peptide sequence
161 <400> SEQUENCE: 8
162 Phe Asn Phe Arg Leu Lys Ala Gly Gln
E--> 163 Lys Ile Arg Phe Gly Gly Gly
164 1 5 *same*
E--> 165 10 15
167 Gly Trp Gln Pro Pro Arg Ala Ile
E--> 169 20
193 <210> SEQ ID NO: 10
194 <211> LENGTH: 10
195 <212> TYPE: PRT
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: Description of Artificial
200 Sequence: Biotinylated
201 fibrin-anti-polymerant peptide
203 <220> FEATURE:
204 <221> NAME/KEY: MOD_RES
205 <222> LOCATION: (1)
206 <223> OTHER INFORMATION: Biotinylated-Gly
208 <220> FEATURE:
209 <221> NAME/KEY: MOD_RES
210 <222> LOCATION: (10)
211 <223> OTHER INFORMATION: AMIDATION
213 <400> SEQUENCE: 10
214 Gly Pro Arg Pro Pro Glu Arg His Gln
E--> 215 Sér
E--> 216 1 5 *same*
E--> 217 10
249 <210> SEQ ID NO: 12
250 <211> LENGTH: 18
251 <212> TYPE: PRT
252 <213> ORGANISM: Artificial Sequence
254 <220> FEATURE:
255 <223> OTHER INFORMATION: Description of Artificial
256 Sequence: Endothelial
257 cell binding lipopeptide
259 <220> FEATURE:
260 <221> NAME/KEY: MOD_RES
261 <222> LOCATION: (1)

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/765,614A

DATE: 06/20/2001
TIME: 11:00:39

Input Set : A:\64990SEQ.WPD8-31.txt.txt
Output Set: N:\CRF3\06202001\I765614A.raw

262 <223> OTHER INFORMATION: 2-n-hexadecylstearyl-Lys
264 <220> FEATURE:
265 <221> NAME/KEY: MOD_RES
266 <222> LOCATION: (18)
267 <223> OTHER INFORMATION: AMIDATION
269 <400> SEQUENCE: 12
270 Lys Leu Ala Leu Lys Leu Ala Leu Lys
E--> 271 Ala Leu Lys Ala Ala Leu Lys
272 1 5 *Name*
E--> 273 10 15
275 Leu Ala
312 <210> SEQ ID NO: 14
313 <211> LENGTH: 13
314 <212> TYPE: PRT
315 <213> ORGANISM: Artificial Sequence
317 <220> FEATURE:
318 <223> OTHER INFORMATION: Description of Artificial
319 Sequence: Lipopeptide
320 with an affinity for
321 endothelial cells
323 <220> FEATURE:
324 <221> NAME/KEY: MOD_RES
325 <222> LOCATION: (1)
326 <223> OTHER INFORMATION: Dipalmitoyl-Lys
328 <220> FEATURE:
329 <221> NAME/KEY: MOD_RES
330 <222> LOCATION: (4)
331 <223> OTHER INFORMATION: Acp
333 <220> FEATURE:
334 <221> NAME/KEY: MOD_RES
335 <222> LOCATION: (13)
336 <223> OTHER INFORMATION: AMIDATION
338 <400> SEQUENCE: 14
W--> 339 Lys Lys Lys Xaa Ile Arg Arg Val Ala
E--> 340 Arg Pro Pro Leu
E--> 341 1 5 *Name*
E--> 342 10
345 <210> SEQ ID NO: 15
346 <211> LENGTH: 14
347 <212> TYPE: PRT
348 <213> ORGANISM: Artificial Sequence
350 <220> FEATURE:
351 <223> OTHER INFORMATION: Description of Artificial
352 Sequence: Lipopeptide
353 comprising an interleukin-1
354 receptor binding
W--> 355 peptide
357 <220> FEATURE:
358 <221> NAME/KEY: MOD_RES

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TECH CENTER 1600/2900

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/765,614A

DATE: 06/20/2001
TIME: 11:00:39

Input Set : A:\64990SEQ.WPD8-31.txt.txt
Output Set: N:\CRF3\06202001\I765614A.raw

359 <222> LOCATION: (1)
360 <223> OTHER INFORMATION: Dipalmitoyl-Lys
362 <400> SEQUENCE: 15
363 Lys Gly Asp Trp Asp Gln Phe Gly Leu
E--> 364 Trp Arg Gly Ala Ala 5 *name*
365 1
E--> 366 10
369 <210> SEQ ID NO: 16
370 <211> LENGTH: 12
371 <212> TYPE: PRT
372 <213> ORGANISM: Artificial Sequence
374 <220> FEATURE:
375 <221> NAME/KEY: MOD_RES
376 <222> LOCATION: (1)
377 <223> OTHER INFORMATION: Dabsyl-Tyr
379 <220> FEATURE:
380 <221> NAME/KEY: MOD_RES
381 <222> LOCATION: (10)
382 <223> OTHER INFORMATION: RGDS chain linked via NH2 group
383 of lysine
385 <220> FEATURE:
386 <223> OTHER INFORMATION: Description of Artificial
387 Sequence:Branched core
388 peptide comprising a dabsylated
389 atherosclerotic
W--> 390 plaque-binding sequence and
W--> 391 RGDS
393 <400> SEQUENCE: 16
394 Tyr Arg Ala Leu Val Asp Thr Leu Lys
E--> 395 Lys Gly Cys 5 *name*
E--> 396 1
E--> 397 10
400 <210> SEQ ID NO: 17
401 <211> LENGTH: 25
402 <212> TYPE: DNA
403 <213> ORGANISM: Artificial Sequence
405 <220> FEATURE:
406 <223> OTHER INFORMATION: Description of Artificial
407 Sequence:Synthetic
408 oligonucleotide
410 <220> FEATURE:
411 <221> NAME/KEY: misc_feature
412 <222> LOCATION: (1)
413 <223> OTHER INFORMATION: Biotinylated
415 <400> SEQUENCE: 17
E--> 416 gaaaggtagt ggggtcgtgt gccgg 25 *see item 1 on Exam Summary Sheet*
417
419 <210> SEQ ID NO: 18
420 <211> LENGTH: 15
421

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/765,614A

DATE: 06/20/2001
TIME: 11:00:39

Input Set : A:\64990SEQ.WPD8-31.txt.txt
Output Set: N:\CRF3\06202001\I765614A.raw

421 <212> TYPE: PRT
422 <213> ORGANISM: Artificial Sequence
424 <220> FEATURE:
425 <223> OTHER INFORMATION: Description of Artificial
426 Sequence:Lipopeptide
427 with affinity for thrombi *thrombin?*
429 <220> FEATURE:
430 <221> NAME/KEY: MOD_RES
431 <222> LOCATION: (1)
432 <223> OTHER INFORMATION: Dipalmitoyl-Lys
434 <220> FEATURE:
435 <221> NAME/KEY: MOD_RES
436 <222> LOCATION: (15)
437 <223> OTHER INFORMATION: AMIDATION
439 <400> SEQUENCE: 18
440 Lys Asn Asp Gly Asp Phe Glu Glu Ile
E--> 441 Pro Glu Glu Tyr Leu Gln *Name*
442 1 5
E--> 443 10 15
680 <210> SEQ ID NO: 27
681 <211> LENGTH: 16
682 <212> TYPE: PRT
683 <213> ORGANISM: Artificial Sequence
685 <220> FEATURE:
686 <223> OTHER INFORMATION: Description of Artificial
687 Sequence:Atherosclerotic
688 plaque-binding peptide
690 <400> SEQUENCE: 27
691 Tyr Ala Lys Phe Arg Glu Thr Leu Glu
E--> 692 Asp Thr Arg Asp Arg Met Tyr *Name*
693 1 5
E--> 694 10 15
697 <210> SEQ ID NO: 28
698 <211> LENGTH: 17
699 <212> TYPE: PRT
700 <213> ORGANISM: Artificial Sequence
702 <220> FEATURE:
703 <223> OTHER INFORMATION: Description of Artificial
704 Sequence:Atherosclerotic
705 plaque-binding peptide
707 <400> SEQUENCE: 28
708 Arg Ala Leu Val Asp Thr Glu Phe Lys
E--> 709 Val Lys Gln Glu Ala Gly Ala *Name*
710 1 5
E--> 711 10 15
713 Lys
718 <210> SEQ ID NO: 29
719 <211> LENGTH: 14
720 <212> TYPE: PRT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/765,614A

DATE: 06/20/2001

TIME: 11:00:39

Input Set : A:\64990SEQ.WPD8-31.txt.txt
Output Set: N:\CRF3\06202001\I765614A.raw

721 <213> ORGANISM: Artificial Sequence
723 <220> FEATURE:
724 <223> OTHER INFORMATION: Description of Artificial
725 Sequence:Thrombus
726 binding peptide
728 <400> SEQUENCE: 29
729 Asn Asp Gly Asp Phe Glu Glu Ile Pro
E--> 730 Glu Glu Tyr Leu Gln *None*
731 1 5
E--> 732 10
751 <210> SEQ ID NO: 31
752 <211> LENGTH: 13
753 <212> TYPE: PRT
754 <213> ORGANISM: Artificial Sequence
756 <220> FEATURE:
757 <223> OTHER INFORMATION: Description of Artificial
758 Sequence:Platelet
759 binding peptide
761 <400> SEQUENCE: 31
762 Pro Leu Tyr Lys Lys Ile Ile Lys Lys
E--> 763 Leu Leu Glu Ser *None*
E--> 764 1 5
E--> 765 10

FM
Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/765,614A

DATE: 06/20/2001

TIME: 11:00:40

Input Set : A:\64990SEQ.WPD8-31.txt.txt
Output Set: N:\CRF3\06202001\I765614A.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application Number
L:46 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:50 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:137 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:146 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
M:332 Repeated in SeqNo=7
L:163 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
M:332 Repeated in SeqNo=8
L:215 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
M:332 Repeated in SeqNo=10
L:230 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:271 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12
M:332 Repeated in SeqNo=12
L:339 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:340 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
M:332 Repeated in SeqNo=14
L:355 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:364 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:15
M:332 Repeated in SeqNo=15
L:390 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:391 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:395 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
M:332 Repeated in SeqNo=16
L:416 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:17
L:441 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:18
M:332 Repeated in SeqNo=18
L:492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:692 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:27
M:332 Repeated in SeqNo=27
L:709 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:28
M:332 Repeated in SeqNo=28
L:730 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:29
M:332 Repeated in SeqNo=29
L:763 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:31
M:332 Repeated in SeqNo=31
L:17 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (25) Counted (31)